

# SEQUENCE LISTING

<110> Rothschild, Max  
Ciobanu, Dan  
Malek, Massoud  
Plastow, Graham

<120> Novel PRKAG3 Alleles and Use of the Same as Genetic Markers for Reproductive and Meat Quality Traits

<130> P04668US3

<150> 60/231045

<151> 2000-09-08

<150> 60/260,239

<151> 2001-01-08

<150> 60/299,111

<151> 2001-06-18

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 1873

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (1) .. (1392)

<400> 1

atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct 48

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala

1 5 10 15

gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala

20 25 30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly

35 40 45

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln

50 55 60

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu

65 70 75 80

gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac 288

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp

85 90 95

PatentIn version 3.0

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly 100 105 110	336
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val 115 120 125	384
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg 130 135 140	432
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met 145 150 155 160	480
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe 180 185 190	576
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220	672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270	816
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285	864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290 295 300	912
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr 305 310 315 320	960
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325 330 335	1008

gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac	1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	
340 345 350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg	1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val	
355 360 365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca	1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	
370 375 380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca	1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr	
385 390 395 400	
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg	1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly	
405 410 415	
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc	1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu	
420 425 430	
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc	1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile	
435 440 445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc	1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	
450 455 460	
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaagggg	1452
gccgtggact cagctctcac ttcccctcag cccacttgct tgggtctggct cttgttcagg	1512
taggctccgc ccggggcccc tggcctcagc atcagcccct cagtctccct gggcaccag	1572
atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt	1632
gaaatctacc agcatcaaga ctcaactgtg gaccactgct ttgtcccatt ctcagctgaa	1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac	1752
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct	1812
gagaatgtcc ctggaaggaa gccagttaat aaaccttggt tggatggaat ttggagagtc	1872
g	1873

<210> 2  
 <211> 464  
 <212> PRT  
 <213> Sus scrofa

<400> 2

Met	Ser	Phe	Leu	Glu	Gln	Gly	Glu	Ser	Arg	Ser	Trp	Pro	Ser	Arg	Ala	1	5	10	15
Val	Thr	Thr	Ser	Ser	Glu	Arg	Ser	His	Gly	Asp	Gln	Gly	Asn	Lys	Ala	20	25	30	
Ser	Arg	Trp	Thr	Arg	Gln	Glu	Asp	Val	Glu	Glu	Gly	Gly	Pro	Pro	Gly	35	40	45	
Pro	Arg	Glu	Gly	Pro	Gln	Ser	Arg	Pro	Val	Ala	Glu	Ser	Thr	Gly	Gln	50	55	60	
Glu	Ala	Thr	Phe	Pro	Lys	Ala	Thr	Pro	Leu	Ala	Gln	Ala	Ala	Pro	Leu	65	70	75	80
Ala	Glu	Val	Asp	Asn	Pro	Pro	Thr	Glu	Arg	Asp	Ile	Leu	Pro	Ser	Asp	85	90	95	
Cys	Ala	Ala	Ser	Ala	Ser	Asp	Ser	Asn	Thr	Asp	His	Leu	Asp	Leu	Gly	100	105	110	
Ile	Glu	Phe	Ser	Ala	Ser	Ala	Ala	Ser	Gly	Asp	Glu	Leu	Gly	Leu	Val	115	120	125	
Glu	Glu	Lys	Pro	Ala	Pro	Cys	Pro	Ser	Pro	Glu	Val	Leu	Leu	Pro	Arg	130	135	140	
Leu	Gly	Trp	Asp	Asp	Glu	Leu	Gln	Lys	Pro	Gly	Ala	Gln	Val	Tyr	Met	145	150	155	160
His	Phe	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser	165	170	175	
Lys	Leu	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe	180	185	190	?
Ala	Leu	Val	Ala	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys	195	200	205	
Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val	210	215	220	
Leu	His	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu	225	230	235	240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe  
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val  
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro  
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys  
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr  
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val  
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val  
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr  
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly  
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
450 455 460

<210> 3

<211> 1873

[illegible]

6

aag Lys	cag Gln	agc Ser	ttc Phe	gtg Val	ggg Gly	atg Met	ctg Leu	acc Thr	atc Ile	aca Thr	gac Asp	ttc Phe	atc Ile	ttg Leu	gtg Val	672
210			215			220										
ctg Leu	cac His	cgc Arg	tat Tyr	tac Tyr	agg Arg	tcc Ser	ccc Pro	ctg Leu	gtc Val	cag Gln	atc Ile	tac Tyr	gag Glu	att Ile	gaa Glu	720
225			230			235										
gaa Glu	cat His	aag Lys	att Ile	gag Glu	acc Thr	tgg Trp	agg Arg	gag Glu	atc Ile	tac Tyr	ctt Leu	caa Gln	ggc Gly	tgc Cys	ttc Phe	768
245			250			255										
aag Lys	cct Pro	ctg Leu	gtc Val	tcc Ser	atc Ile	tct Ser	ccc Pro	aat Asn	gac Asp	agc Ser	ctg Leu	ttc Phe	gaa Glu	gct Ala	gtc Val	816
260			265			270										
tac Tyr	gcc Ala	ctc Leu	atc Ile	aag Lys	aac Asn	cgg Arg	atc Ile	cac His	cgc Arg	ctg Leu	ccg Pro	gtc Val	ctg Leu	gac Asp	cct Pro	864
275			280			285										
gtc Val	tcc Ser	ggg Gly	gct Ala	gtg Val	ctc Leu	cac His	atc Ile	ctc Leu	aca Thr	cat His	aag Lys	cgg Arg	ctt Leu	ctc Leu	aag Lys	912
290			295			300										
ttc Phe	ctg Leu	cac His	atc Ile	ttt Phe	ggc Gly	acc Thr	ctg Leu	ctg Leu	ccc Pro	cgg Arg	ccc Pro	tcc Ser	ttc Phe	ctc Leu	tac Tyr	960
305			310			315										
cgc Arg	acc Thr	atc Ile	caa Gln	gat Asp	ttg Leu	ggc Gly	atc Ile	ggc Gly	aca Thr	ttc Phe	cga Arg	gac Asp	ttg Leu	gcc Ala	gtg Val	1008
325			330			335										
gtg Val	ctg Leu	gaa Glu	acg Thr	gcg Ala	ccc Pro	atc Ile	ctg Leu	acc Thr	gca Ala	ctg Leu	gac Asp	atc Ile	ttc Phe	gtg Val	gac Asp	1056
340			345			350										
cgg Arg	cgt Arg	gtg Val	tct Ser	gcg Ala	ctg Leu	cct Pro	gtg Val	gtc Val	aac Asn	gaa Glu	act Thr	gga Gly	cag Gln	gta Val	gtg Val	1104
355			360			365										
ggc Gly	ctc Leu	tac Tyr	tct Ser	cgc Arg	ttt Phe	gat Asp	gtg Val	atc Ile	cac His	ctg Leu	gct Ala	gcc Ala	caa Gln	caa Gln	aca Thr	1152
370			375			380										
tac Tyr	aac Asn	cac His	ctg Leu	gac Asp	atg Met	aat Asn	gtg Val	gga Gly	gaa Glu	gcc Ala	ctg Leu	agg Arg	cag Gln	cgg Arg	aca Thr	1200
385			390			395										
ctg Leu	tgt Cys	ctg Leu	gaa Glu	ggc Gly	gtc Val	ctt Leu	tcc Ser	tgc Cys	cag Gln	ccc Pro	cac His	gag Glu	acc Thr	ttg Leu	ggg Gly	1248
405			410			415										
gaa Glu	gtc Val	att Ile	gac Asp	cgg Arg	att Ile	gtc Val	cgg Arg	gaa Glu	cag Gln	gtg Val	cac His	cgc Arg	ctg Leu	gtg Val	ctc Leu	1296
420			425			430										
gtg Val	gat Asp	gag Glu	acc Thr	cag Gln	cac His	ctt Leu	ctg Leu	ggc Gly	gtg Val	gtg Val	tcc Ser	ctc Leu	tct Ser	gac Asp	atc Ile	1344

435	440	445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc			1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala			
450	455	460	
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga			1452
gccgtggact cagctctcac ttcccctcag ccccaacttgc tggctctggct cttgttcagg			1512
taggctccgc ccggggcccc tggcctcagc atcagcccct cagtctccct gggcaccag			1572
atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt			1632
gaaatctacc agcatcaaga ctcaactgtgg gaccactgct ttgtcccatt ctcagctgaa			1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac			1752
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct			1812
gagaatgtcc ctggaaggaa gccagttaat aaaccttggt tggatggaat ttggagagtc			1872
g			1873
<210> 4			
<211> 464			
<212> PRT			
<213> Sus scrofa			
<400> 4			
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala			
1 5 10 15			
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Thr Lys Ala			
20 25 30			
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly			
35 40 45			
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln			
50 55 60			
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu			
65 70 75 80			
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp			
85 90 95			
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly			
100 105 110			





Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val  
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr  
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly  
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
450 455 460

<210> 5  
<211> 1873  
<212> DNA  
<213> Sus scrofa  
  
<220>  
<221> CDS  
<222> (1)..(1392)

<400> 5  
atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct 48  
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
1 5 10 15  
  
gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96  
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
20 25 30  
  
tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144  
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly  
35 40 45  
  
ccg agg gaa agt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192  
Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
50 55 60  
  
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240  
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
65 70 75 80

gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac	288
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp	
85 90 95	
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc	336
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	
100 105 110	
ata gag ttc tca gcc tcc gcg gcg tcc ggg gat gag ctt ggg ctg gtg	384
Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val	
115 120 125	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg	432
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	
130 135 140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg	480
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	
145 150 155 160	
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc	528
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
195 200 205	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg	672
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
210 215 220	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa	720
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc	768
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
245 250 255	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct	864
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag	912
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	
290 295 300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac	960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	

305	310	315	320	
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg				1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val				
	325	330	335	
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac				1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp				
	340	345	350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg				1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val				
	355	360	365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca				1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr				
	370	375	380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca				1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr				
	385	390	395	400
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg				1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly				
	405	410	415	
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc				1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu				
	420	425	430	
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc				1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile				
	435	440	445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc				1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala				
	450	455	460	
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga				1452
gccgtggact cagctctcac ttccctcag cccacttgc tggctctggct cttgttcagg				1512
taggctccgc ccggggcccc tggcctcagc atcagcccct cagtctccct gggcaccag				1572
atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt				1632
gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtcccatt ctcagctgaa				1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac				1752
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct				1812
gagaatgtcc ctggaaggaa gccagttaat aaaccttggg ttgatggaat ttggagagtc				1872
g				1873

<210> 6  
<211> 464

Kategorie		Anzahl		Prozent	
Gesamt	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Unterschiede	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Gesamt	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Unterschiede	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Gesamt	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Unterschiede	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Gesamt	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Unterschiede	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Gesamt	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100
Unterschiede	1. Gruppe	100	100	100	100
	2. Gruppe	100	100	100	100
	3. Gruppe	100	100	100	100
	4. Gruppe	100	100	100	100

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val  
210 215 220



450

455

460

<210> 7  
<211> 1873  
<212> DNA  
<213> Sus scrofa

<220>  
<221> CDS  
<222> (1) .. (1392)

<400> 7  
atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct 48  
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
1 5 10 15  
  
gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96  
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
20 25 30  
  
tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144  
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly  
35 40 45  
  
ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192  
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
50 55 60  
  
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240  
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
65 70 75 80  
  
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac 288  
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
85 90 95  
  
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc 336  
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
100 105 110  
  
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg 384  
Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val  
115 120 125  
  
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg 432  
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
130 135 140  
  
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg 480  
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met  
145 150 155 160  
  
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc 528  
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser  
165 170 175  
  
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt 576  
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe

180	185	190	
gcc ctg gtg gcc aac ggc atc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205			624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220			672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240			720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255			768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270			816
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285			864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290 295 300			912
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr 305 310 315 320			960
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325 330 335			1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340 345 350			1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355 360 365			1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370 375 380			1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385 390 395 400			1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405 410 415			1248
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc			1296



Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc 1344  
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
435 440 445

ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc 1392  
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
450 455 460

tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga 1452

gccgtggact cagctctcac ttcccctcag cccacttgc tggctctggct cttgttcagg 1512

taggctccgc ccggggcccc tggcctcagc atcagcccct cagtctccct gggcaccag 1572

atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt 1632

gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtcccatt ctcagctgaa 1692

atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtac 1752

gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct 1812

gagaatgtcc ctggaaggaa gccagttaat aaaccttggt tggatggaat ttggagagtc 1872

g 1873

<210> 8  
<211> 464  
<212> PRT  
<213> Sus scrofa

<400> 8

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly  
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
85 90 95





50	55	60	
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu 65 70 75 80	240		
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp 85 90 95	288		
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly 100 105 110	336		
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val 115 120 125	384		
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg 130 135 140	432		
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met 145 150 155 160	480		
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528		
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe 180 185 190	576		
gcc ctg gtg gcc aac ggc gtc caa gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624		
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220	672		
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720		
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768		
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260 265 270	816		
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285	864		
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag	912		

Val	Ser	Gly	Ala	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys	
290						295					300					
ttc	ctg	cac	atc	ttt	ggc	acc	ctg	ctg	ccc	cgg	ccc	tcc	ttc	ctc	tac	960
Phe	Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr	
305					310					315					320	
cgc	acc	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gcc	gtg	1008
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val	
				325					330						335	
gtg	ctg	gaa	acg	gcg	ccc	atc	ctg	acc	gca	ctg	gac	atc	ttc	gtg	gac	1056
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp	
				340					345						350	
cgg	cgt	gtg	tct	gcg	ctg	cct	gtg	gtc	aac	gaa	act	gga	cag	gta	gtg	1104
Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Thr	Gly	Gln	Val	Val	
		355					360					365				
ggc	ctc	tac	tct	cgc	ttt	gat	gtg	atc	cac	ctg	gct	gcc	caa	caa	aca	1152
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr	
		370				375					380					
tac	aac	cac	ctg	gac	atg	aat	gtg	gga	gaa	gcc	ctg	agg	cag	cgg	aca	1200
Tyr	Asn	His	Leu	Asp	Met	Asn	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr	
385					390					395					400	
ctg	tgt	ctg	gaa	ggc	gtc	ctt	tcc	tgc	cag	ccc	cac	gag	acc	ttg	ggg	1248
Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Thr	Leu	Gly	
				405						410					415	
gaa	gtc	att	gac	cgg	att	gtc	cgg	gaa	cag	gtg	cac	cgc	ctg	gtg	ctc	1296
Glu	Val	Ile	Asp	Arg	Ile	Val	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu	
				420					425						430	
gtg	gat	gag	acc	cag	cac	ctt	ctg	ggc	gtg	gtg	tcc	ctc	tct	gac	atc	1344
Val	Asp	Glu	Thr	Gln	His	Leu	Leu	Gly	Val	Val	Ser	Leu	Ser	Asp	Ile	
			435				440								445	
ctt	cag	gct	ctg	gtg	ctc	agc	cct	gct	gga	att	gat	gcc	ctc	ggg	gcc	1392
Leu	Gln	Ala	Leu	Val	Leu	Ser	Pro	Ala	Gly	Ile	Asp	Ala	Leu	Gly	Ala	
			450				455								460	
tgagaacctt	ggaacctttg	ctctcaggcc	acctggcaca	cctggaagcc	agtgaaggga											1452
gccgtggact	cagctctcac	ttccctcag	cccacttgc	tggtctggct	cttggtcagg											1512
taggctccgc	ccggggcccc	tggcctcagc	atcagcccct	cagtctccct	gggcacccag											1572
atctcagact	ggggcaccct	gaagatggga	gtggcccagc	ttatagctga	gcagccttgt											1632
gaaatctacc	agcatcaaga	ctcactgtgg	gaccactgct	ttgtcccatt	ctcagctgaa											1692
atgatggagg	gcctcataag	aggggtggac	agggcctgga	gtagaggcca	gatcagtgac											1752
gtgccttcag	gacctccggg	gagttagagc	tgccctctct	cagttcagtt	ccccctgct											1812
gagaatgtcc	ctggaaggaa	gccagttaat	aaaccttggt	tggatggaat	ttggagagtc											1872

<210> 10  
 <211> 464  
 <212> PRT  
 <213> Sus scrofa

<400> 10

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
 1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
 20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly  
 35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
 50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
 65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
 85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
 100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val  
 115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
 130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met  
 145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser  
 165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe  
 180 185 190

Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys

205

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
 435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
 450 455 460

<210> 11  
 <211> 1095  
 <212> DNA  
 <213> Sus scrofa

<400> 11  
 gaaactcttc tccccacaga ctccctcctg gagcagcctc gggggaccta agcatcaagg 60  
 taggtggggc tgccccctgct cgcgggcccc ggctcttctc ccacctcctt ttcttccacg 120  
 tcttcaggac cccaatctcc cccaactccac tcgcctggct cttgtcttcc tctcctttgc 180  
 cttctttgtt ccgctttgtt tcttcttcct ccctctccct cacctcctcc ctctttcaaa 240  
 agagtagagg gggcatctat agagtctgga gattgggact ctcttgactt tctcgcttac 300  
 tagctgtgtg atttgtggca aattgcttca cctctctgag ctcaggctctc tcgttagtaa 360  
 aacagggctg atagccatgc ccttcggata agattgccgt gaggggtgaa tgagaaattt 420  
 gttggaggac aagccctttg aagcttcccc atattaaata tttttattta tttatttatt 480  
 ttttgtcttt ttgctattcc tttgggccgc tcccacggca tatggagggtt cccaggctag 540  
 gggtcgaatc ggagctgtag cactggcct acgccagagc cacagcaacg cgggatccga 600  
 gccgcatctg caacctacac cacagctcac ggcaacgccg gatcggttaac ccactgagca 660  
 ggggcaggca ccgaacctgc aacctcatgg ttcttagtgg gattcggttaa ccactgcgcc 720  
 acgacgggaa ctcccccaata ttaaataatta ttattagtaa cattttaatg gaatttattg 780  
 tgttactccc cattaaccaa acagggtcca ttctcccttg cagagatgag cttcctagag 840  
 caaggagaga gccgttcatg gccatcccg gctgtgacca ccagctcaga aagaagccat 900  
 ggggaccagg ggaccaaggc ctctagatgg acaaggcagg aggatrtaga ggaagggggg 960  
 cctccggggc cgaggggaarg tgagttcaag gccagttctg gggagctggg actggggggca 1020  
 gtgggcagtc ctcaaacctg gggcccgtct ctggtctggt ccctccataa cacaggcaca 1080  
 taacatcatg cagcc 1095

<210> 12  
 <211> 808  
 <212> DNA  
 <213> Sus scrofa

<400> 12





<213> Sus scrofa

<400> 16

ggagcaaagtg tgcagacaag

20

<210> 17

<211> 20

<212> DNA

<213> Sus scrofa

<400> 17

cccacgaagc tctgcttctt

20